

PAGE: 1

07/30/97
RAW SEQUENCE LISTING
PATENT APPLICATION US/08/862,442DATE: 07/30/97
TIME: 10:42:39

INPUT SET: S19288.raw

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Claude
10011
This Raw Listing contains the General
Information Section and up to the first 5 pages.

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SEQUENCE LISTING

1
2
3 (1) General Information:4
5 (i) APPLICANT: Shyjan, Andrew W.6
7 (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
8 DIAGNOSIS, PREVENTION AND TREATMENT OF TUMOR
9 PROGRESSION10
11 (iii) NUMBER OF SEQUENCES: 912
13 (iv) CORRESPONDENCE ADDRESS:14 (A) ADDRESSEE: Fish & Richardson P.C.
15 (B) STREET: 225 Franklin Street
16 (C) CITY: Boston
17 (D) STATE: MA
18 (E) COUNTRY: USA
19 (F) ZIP: 02110-280420
21 (v) COMPUTER READABLE FORM:22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.3026
27 (vi) CURRENT APPLICATION DATA:28 (A) APPLICATION NUMBER:
29 (B) FILING DATE: 23-MAY-1997
30 (C) CLASSIFICATION:31
32 (vii) PRIOR APPLICATION DATA:33 (A) APPLICATION NUMBER: 08/623,679
34 (B) FILING DATE: 29-MAR-199635
36 (viii) PRIOR APPLICATION DATA:37 (A) APPLICATION NUMBER: 08/412,431
38 (B) FILING DATE: 29-MAR-199539
40 (ix) ATTORNEY/AGENT INFORMATION:41 (A) NAME: Fasse, J. Peter
42 (B) REGISTRATION NUMBER: 32,983
43 (C) REFERENCE/DOCKET NUMBER: 07334/00400244
45 (x) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: 617/542-5070

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47 (B) TELEFAX: 617/542-8906
48 (C) TELEX: 200154

49
50 (2) INFORMATION FOR SEQ ID NO:1:

51
52 (i) SEQUENCE CHARACTERISTICS:
53 (A) LENGTH: 186 base pairs
54 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
56 (D) TOPOLOGY: linear

57
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

59
60 GGTGCTGGAG TACCTCATGG GCGGTGCCTA CCGCTGCAAC TACACTCGGA AAAGCTTCCG 60
61
62 GACTCTCTAC AACAACTTGT TTGGCCCTAA GAGGGTAGAG CTCAGCAGAC ACACAGTGTC 120
63
64 CTGTGCCTCC CAGAGTAACA TGTGGTTCCCT TGATGTGCTT CCCCAAAAGC CCACCTGTGC 180
65
66 AGAATG 186
67

68 (2) INFORMATION FOR SEQ ID NO:2:

69
70 (i) SEQUENCE CHARACTERISTICS:
71 (A) LENGTH: 2729 base pairs
72 (B) TYPE: nucleic acid
73 (C) STRANDEDNESS: single
74 (D) TOPOLOGY: linear

75
76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

77
78 AAGGAGGCTA GGCTGCACCC TTCCCGCTTG CTCAGCAGCT GAGGCAGGGT CAGAAAGCAT 60
79
80 GGATAGAGAA GACATTTGC AAAAGGAAT GCATCTTGT AATTCCAGT ACAAAAGACC 120
81
82 CTAACAGATG TTGCTGTGGT CAGCTCACTA ACCAGCACAT CCCCCCTTTG CCGAGTGGGG 180
83
84 CTCCCAGCAC AACAGGAGAG GACACCAAGC AGGCAGACAC GCAGTCCGGG AAATGGTCTG 240
85
86 TCAGCAAACA CACCCAGAGC TACCCAACAG ACTCCTATGG GATTCTTGAA TTCCAGGGTG 300
87
88 GGGGTTACTC CAATAAAGCC ATG TAC ATC CGA GTC TCC TAC GAC ACC AAG 350
89 Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys
90 1 5 10
91
92 CCA GAT TCC CTG CTC CAC CTC ATG GTG AAG GAC TGG CAG CTG GAG CTC 398
93 Pro Asp Ser Leu Leu His Leu Met Val Lys Asp Trp Gln Leu Glu Leu
94 15 20 25
95
96 CCG AAG CTC TTG ATA TCT GTG CAC GGA GGC CTC CAA AGC TTC GAG ATG 446
97 Pro Lys Leu Leu Ile Ser Val His Gly Gly Leu Gln Ser Phe Glu Met
98 30 35 40
99

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100	CAG TCC AAA CTG AAG CAG GTG TTT GGG AAA GGT CTG ATC AAG GCT GCC	494		
101	Gln Ser Lys Leu Lys Gln Val Phe Gly Lys Gly Leu Ile Lys Ala Ala			
102	45	50	55	
103				
104	ATG ACC ACG GGG GCG TGG ATC TTC ACC GGG GGT GTG AGC ACT GGT GTC	542		
105	Met Thr Thr Gly Ala Trp Ile Phe Thr Gly Gly Val Ser Thr Gly Val			
106	60	65	70	
107				
108	GTC AGC CAT GTG GGG GAT GCC TTG AAA GAC CAC TCC TCC AAG TCC AGA	590		
109	Val Ser His Val Gly Asp Ala Leu Lys Asp His Ser Ser Lys Ser Arg			
110	75	80	85	90
111				
112	GGC CGG CTC TGT GCT ATA GGA ATT GCT CCC TGG GGC ATG GTG GAG AAC	638		
113	Gly Arg Leu Cys Ala Ile Gly Ile Ala Pro Trp Gly Met Val Glu Asn			
114	95	100	105	
115				
116	AAG GAA GAC CTG ATT GGA AAA GAT GTA ACA AGA GTC TAT CAG ACC ATG	686		
117	Lys Glu Asp Leu Ile Gly Lys Asp Val Thr Arg Val Tyr Gln Thr Met			
118	110	115	120	
119				
120	TCC AAC CCT CTG AGC AAG CTC TCT GTG CTC AAC AAT TCC CAC ACT CAC	734		
121	Ser Asn Pro Leu Ser Lys Leu Ser Val Leu Asn Asn Ser His Thr His			
122	125	130	135	
123				
124	TTC ATC TTG GCT GAC AAC GGC ACC CTG GGC AAG TAT GGT GCT GAG GTG	782		
125	Phe Ile Leu Ala Asp Asn Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val			
126	140	145	150	
127				
128	AAG CTT CGA AGA CAG CTG GAA AAA CAC ATC TCC CTG CAG AAG ATC AAC	830		
129	Lys Leu Arg Arg Gln Leu Glu Lys His Ile Ser Leu Gln Lys Ile Asn			
130	155	160	165	170
131				
132	ACA AGG CTG GGC CAG GGT GTA CCT GTC GTG GGC CTA GTG GTA GAA GGT	878		
133	Thr Arg Leu Gly Gln Gly Val Pro Val Val Gly Leu Val Val Glu Gly			
134	175	180	185	
135				
136	GGT CCT AAC GTG GTT TCT ATC GTC CTG GAG TAT CTC AAA GAA GAC CCT	926		
137	Gly Pro Asn Val Val Ser Ile Val Leu Glu Tyr Leu Lys Glu Asp Pro			
138	190	195	200	
139				
140	CCT GTC CCT GTG GTT TGC GAT GGC AGT GGA CGT GCC TCT GAC ATT	974		
141	Pro Val Pro Val Val Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile			
142	205	210	215	
143				
144	TTG TCC TTC GCA CAC AAA TAC TGC GAC GAA GGA GGA GTC ATA AAC GAG	1022		
145	Leu Ser Phe Ala His Lys Tyr Cys Asp Glu Gly Val Ile Asn Glu			
146	220	225	230	
147				
148	TCC CTG CGG GAC CAG CTT CTA GTT ACC ATT CAG AAA ACA TTT AAT TAC	1070		
149	Ser Leu Arg Asp Gln Leu Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr			
150	235	240	245	250
151				
152	AGC AAG TCC CAG TCG TAT CAG CTG TTT GCA ATT ATC ATG GAG TGC ATG	1118		

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153	Ser Lys Ser Gln Ser Tyr Gln Leu Phe Ala Ile Ile Met Glu Cys Met			
154	255	260	265	
155				
156	AAG AAG AAA GAA CTC GTC ACT GTG TTT CCG ATG GGT TCC GAG GGT CAG		1166	
157	Lys Lys Lys Glu Leu Val Thr Val Phe Arg Met Gly Ser Glu Gly Gln			
158	270	275	280	
159				
160	CAA GAT GTC GAG ATG GCA ATT TTA ACT GCC TTG CTC AAA GGA ACC AAC		1214	
161	Gln Asp Val Glu Met Ala Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn			
162	285	290	295	
163				
164	GCA TCA GCT CCA GAT CAG CTG AGC TTG GCC CTG GCT TGG AAC CGG GTC		1262	
165	Ala Ser Ala Pro Asp Gln Leu Ser Leu Ala Leu Ala Trp Asn Arg Val			
166	300	305	310	
167				
168	GAC ATA GCG CGA AGC CAG ATC TTC GTC TTT GGC CCA CAC TGG CCG CCA		1310	
169	Asp Ile Ala Arg Ser Gln Ile Phe Val Phe Gly Pro His Trp Pro Pro			
170	315	320	325	330
171				
172	CTG GGA AGC CTG GCC CCT CCT GTG GAC ACC AAA GCC GCA GAG AAG GAA		1358	
173	Leu Gly Ser Leu Ala Pro Pro Val Asp Thr Lys Ala Ala Glu Lys Glu			
174	335	340	345	
175				
176	AAG AAG CCA CCC ACA GCC ACC ACC AAG GGG AGA GGA AAA GGA AAA GGC		1406	
177	Lys Lys Pro Pro Thr Ala Thr Thr Lys Gly Arg Gly Lys Gly Lys Gly			
178	350	355	360	
179				
180	AAG AAG AAA GGC AAA GTG AAA GAG GAA GTG GAG GAA GAG ACG GAC CCC		1454	
181	Lys Lys Gly Lys Val Lys Glu Glu Val Glu Glu Glu Thr Asp Pro			
182	365	370	375	
183				
184	CGG AAG CTT GAG CTG CTC AAC TGG GTG AAT GCC CTG GAG CAA GCC ATG		1502	
185	Arg Lys Leu Glu Leu Leu Asn Trp Val Asn Ala Leu Glu Gln Ala Met			
186	380	385	390	
187				
188	CTG GAT GCT CTT GTC CTA GAT CGG GTG GAC TTT GTA AAG CTC CTG ATT		1550	
189	Leu Asp Ala Leu Val Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile			
190	395	400	405	410
191				
192	GAA AAC GGA GTG AAC ATG CAG CAT TTC CTC ACC ATC CCG AGG CTG GAG		1598	
193	Glu Asn Gly Val Asn Met Gln His Phe Leu Thr Ile Pro Arg Leu Glu			
194	415	420	425	
195				
196	GAG CTA TAC AAC ACC AGA CTG GGC CCA CCA AAC ACC CTT CAT CTG CTG		1646	
197	Glu Leu Tyr Asn Thr Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu			
198	430	435	440	
199				
200	GTG CGG GAT GTA AAG AAG AGC AAC CTT CCA CCT GAT TAC CAC ATC AGC		1694	
201	Val Arg Asp Val Lys Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser			
202	445	450	455	
203				
204	CTC ATT GAT ATA GGA CTG GTG CTG GAG TAC CTC ATG GGC GGT GCC TAC		1742	
205	Leu Ile Asp Ile Gly Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr			

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206	460	465	470	
207				
208	CGC TGC AAC TAC ACT CGG AAA AGC TTC CGG ACT CTC TAC AAC AAC TTG			1790
209	Arg Cys Asn Tyr Thr Arg Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu			
210	475	480	485	490
211				
212	TTT GGC CCT AAG AGG GTA GAG CTC AGC AGA CAC ACA GTG TCC TGT GCC			1838
213	Phe Gly Pro Lys Arg Val Glu Leu Ser Arg His Thr Val Ser Cys Ala			
214	495	500		505
215				
216	TCC CAG AGT AAC ATG TGG TTC CTT GAT GTG CTT CCC CAA AAG CCC ACC			1886
217	Ser Gln Ser Asn Met Trp Phe Leu Asp Val Leu Pro Gln Lys Pro Thr			
218	510	515		520
219				
220	TGT GCA GAA TGC AAC TCT TCA CCT CAC CTG TCC CAA ACT GAC ATC ACC			1934
221	Cys Ala Glu Cys Asn Ser Ser Pro His Leu Ser Gln Thr Asp Ile Thr			
222	525	530		535
223				
224	CCA CCT CTG CCC T GACACCCAGT GCAGGGCCTC CTAGCTTCA CATGCAGCCA			1987
225	Pro Pro Leu Pro			
226	540			
227				
228	TTCACATCGC CTCTCAAGAC TGGGCCAGGC AGTGCAACCT GTCAAGCATG TCTGTCCTCC			2047
229				
230	CCTCCCTCCT ACAATAGCCC CCCCTCTGGG CCCCATGCCT CTGCTCTCTC AGCCCGTTCT			2107
231				
232	CCTCCCCACT GATCACTGGC GCTCCTGTTG TCTTCCAAGG CAAGGAACAA GGAAAAGCAT			2167
233				
234	CTTTTGCCC ACAAAAGTTT AGGGCTCCCC GCTGTTCAAC CATAGCCAAC CTCACTGTAC			2227
235				
236	ATCGGAGTCA TCCAGGCCAG CTGCCACACA CAAGCCTTCC CCACCCCTATC CCAATAGACC			2287
237				
238	CTATTCCCTCC ATCAAAATCA AAGCTAACTC CTGGCCTGCC ACATTGCTTC TTCTTGCTCC			2347
239				
240	AGCCTGTTAA ACCTCCAATA AATGTCAGAT CTGTGGGAAG CCTTCCTCAC TCTCACTCCA			2407
241				
242	CAGTTGTAC AGAGAGCCAG AGCCTCGTTT GGTTCTACTT ACAAGGAAGG CTTTGTGTCT			2467
243				
244	GTCTGTCCTT CCCAACTGAC TTCTGTTGAC AGAACGACTT TCCACATGAA AGCGTTGACT			2527
245				
246	CACCTGGATG TTGTCATTAA TTAATAGTGA TACAAAATAT TGACACTTCT TTTCCTGCTT			2587
247				
248	CTTTGTTATG CAGCCGAAAG CACTTAAGCT TCTGGGAATG GAAGTAAGTA GGACATGTTT			2647
249				
250	GTGGCAGTTT ATTTACTATA TATACTTTG TCATTCTGTG GAAGAAAAA TTGCAATGTT			2707
251				
252	TTCCATGAAT AAAGCTCGTG CC	◆		2729
253				
254		◆		
255				
256	(2) INFORMATION FOR SEQ ID NO:3:			
257				
258	(i) SEQUENCE CHARACTERISTICS:			

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/862,442

DATE: 07/30/97
TIME: 10:42:50

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